

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2002, 21:05:13 ; Search time 11 Seconds

(without alignments)
813.111 million cell updates/sec

Title: US-09-840-795-19

Perfect score: 1273

Sequence: 1 MDCQENYWDQRCVTCQR.....AQLFSIDSVIPQDQGPDM 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Result No. Score Match Query Length DB ID Description

Result No.	Score	Match	Query Length	DB ID	Description
1	153.5	12.1	260	1	TNFR_HUMAN
2	152.5	12.0	415	1	TNFR_MOUSE
3	145.5	11.4	455	1	TRIA_HUMAN
4	145.5	11.4	454	1	TRIA_MOUSE
5	143.5	11.3	250	1	TNFR_MOUSE
6	143	11.2	332	1	TNFR_PIG
7	142	11.2	625	1	TR11_MOUSE
8	141.5	11.1	283	1	TR14_HUMAN
9	134.5	10.6	323	1	TNFR_BOVIN
10	134.5	10.6	461	1	TR1A_PIG
11	134.5	10.6	471	1	TR1A_BOVIN
12	134	10.5	435	1	TNFR_HUMAN
13	132.5	10.4	461	1	TR1A_HUMAN
14	130	10.2	461	1	TR1A_RAT
15	129.5	10.2	256	1	TNFR_MOUSE
16	129.5	10.2	327	1	TNFR_MOUSE
17	124.5	9.8	255	1	TNFR_HUMAN
18	124	9.7	616	1	TR11_HUMAN
19	122	9.6	1006	1	EPB6_MOUSE
20	121	9.5	324	1	TNFR_RAT
21	119	9.3	335	1	TNRE_HUMAN
22	118	9.3	474	1	TR1B_MOUSE
23	117	9.2	417	1	TR12_HUMAN
24	116.5	9.2	416	1	TR16_CHICK
25	114.5	9.0	326	1	TNRA_RAT
26	114.5	9.0	326	1	VT2_MYXVL
27	111	8.7	272	1	TNRA_MOUSE
28	110.5	8.7	1639	1	LMG1_DROME
29	108	8.5	814	1	AD15_HUMAN
30	108	8.5	1877	1	PCRS_MOUSE
31	107.5	8.4	269	1	TNRS_BOVIN
32	107.5	8.4	2569	1	LM3_MOUSE
33	107	8.4	440	1	T10B_HUMAN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

ALIGNMENTS

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

Result ID	Score	Match	Query Length	DB ID	Description
1	107	8.4	1014	1	EPB6_MOUSE
2	106	8.3	1696	1	PCRS_BRACL
3	106	8.3	2813	1	VWF_CANPA
4	104.5	8.2	3695	1	LM3_HUMAN
5	103.5	8.1	3718	1	LM45_MOUSE
6	102.5	8.1	425	1	TR16_RAT
7	101.5	8.0	349	1	VC22_VARV
8	101	7.9	3084	1	LM41_MOUSE
9	100	7.9	277	1	TNRS_HUMAN
10	100	7.9	595	1	TNRS_HUMAN
11	100	7.9	3075	1	LM41_HUMAN
12	98	7.7	3075	1	LM41_HUMAN
13	97.5	7.7	277	1	TNRA_HUMAN

RESULT 1			
ID	TNFR7_HUMAN	STANDARD:	PRT: 260 AA.
AC	P26842.2		
DT	01-AUG-1992	(Rel. 23, Created)	
DT	01-AUG-1992	(Rel. 23, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	Tumor necrosis factor receptor superfamily member 7 precursor (CD27L receptor) (T-cell activation antigen CD27) (T14).		
GN	TNFRSF7 OR CD27.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Monocytes;		
RX	MEDLINE=92031149; PubMed=1655907;		
RA	Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.;		
RT	"The T cell activation antigen CD27 is a member of the nerve growth factor/tumor necrosis factor receptor gene family.";		
RL	J. Immunol. 147:3165-3169(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93094588; PubMed=1334106;		
RA	Loenen W.A., Gravesstein L.A., Beumer S., Melief C.J., Hagemeijer A., Borst J.;		
RT	"Genomic organization and chromosomal localization of the human CD27 gene.";		
RL	J. Immunol. 149:3937-3943(1992).		
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.		
CC	-1- SUBUNIT: HOMODIMER.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- TISSUE SPECIFICITY: FOUND IN MOST T LYMPHOCYTES.		
CC	-1- PFM: PHOSPHORYLATED AND O-GLYCOSYLATED (PROBABLE).		
CC	-1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.		
CC	-1- DATABASE: NAME=PRO; NOTE=CD guide CD27 entry.		
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd27.htm".		
CC	-----		
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; M63928; AAA58411.1; .		
DR	PIR; A46454; A46454.		
DR	PIR; A46517; A46517.		
DR	HSSP; P19438; 1TNR.		
DR	MM; 186711; .		
DR	InterPro; IPR001368; TNFR_C6.		
DR	Pfam; PF00020; TNFR_C6; 2.		
DR	ProDom; PD000771; TNFR_C6; 1.		

```

DR SMART: SM00208; TNFR. 2.
DR PROSITE: PS00652; TNFR_NGFR.1; 1.
DR PROSITE: PS00650; TNFR_NGFR.2; 1.
KW T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW Phosphorylation.
FT CHAIN 1 20
FT CHAIN 21 260
FT DOMAIN 21 191
FT TRANSMEM 192 212
FT DOMAIN 213 260
FT REPEAT 26 63
FT REPEAT 64 104
FT REPEAT 105 141
FT CARBOHYD 95 95
FT MOD_RES 219 219
FT CONFLICT 59 59
SQ SEQUENCE 260 AA; 29156 MW; 43C38B92FA90D4E2 CRC64;

Query Match 12.1%; Score 153.5; DB 1; Length 260;
Best Local Similarity 25.9%; Pred. No. 2e-06; Mismatches 78; Indels 99; Gaps 18;
Matches 72; Conservative 29;

OY 3 COBNEYWDGRCVTCQRCGQELSKDCGYEGGDVCTACPPRRYKSSGHH--KCQ 59
DB 27 CERNHYWAGKLC--COMCEPGLFKDCDQHRKA-AQCDCPIP-GVSPSPDHTPHCE 82
OY 60 SCITC--AVINRYQVNCATSNANVCG-----DCLPRFYRKTRIGLDQCEIPCK-QT 111
DB 83 SCRHCNSGLIVR---NCTITANABECACRNGWC-----RKECTEDDPLPN 125
OY 112 PSEVQCAFOLS-----LVEN-----DAPYV-----PROEA-- 137
DB 126 PSITARRSQALSPHPQPTLPIVSEMLEARFAGHMOTLADFPRLARTLSTWMPQRSIC 185
OY 138 -----TIVAVLSSLVVFTLALGLFLYCKQFENRHCORGLDLPADKAKESLPPV 192
DB 186 SSDFTRLIVTFSGMFLVFLA--GALFLHQRRKY-----RSNKGES--PV 226
OY 193 PPSKETSAESQVSWAPGSLAQLFSLDSVPIPOOQGP 230
DB 227 EPA-EPCRRYSCPREBGS-----TIPIDRYRKP 255

RESULT 2
ID TNR3_MOUSE STANDARD; PRT: 415 AA.
AC P50284:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lymphotoxin-beta receptor precursor.
GN LTR OR TNCR OR TNRSF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-CVB; TISSUE-Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288(1995).
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";

```

```

RL Genomics 30:312-319(1995).
CC -I- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U29173; AAA68964.1; -
DR EMBL: L38423; AAB00846.1; -
DR EMBL: U30798; AAB81334.1; -
DR HSSP: P25942; 1CDF.
DR MCD; MGI:104875; LtDr.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR. 3.
DR PROSITE: PS00652; TNFR_NGFR.1; 2.
DR PROSITE: PS00650; TNFR_NGFR.2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT CHAIN 1 30
FT DOMAIN 31 415
FT TRANSMEM 31 223
FT DOMAIN 224 244
FT TRANSMEM 245 415
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 59 58
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

Query Match 12.0%; Score 152.5; DB 1; Length 415;
Best Local Similarity 25.3%; Pred. No. 3.e-06; Mismatches 99; Indels 89; Gaps 20;
Matches 74; Conservative 31;

OY 4 QENBYWDGRCVTCQRCGQELSKDCGYEGGDVCTACPPRRYKSSGHH--HKQSCI 62
DB 46 QDKREYEPM-HDVCCSRCPGEFVFAVCSRSQ--DYVCKTCRPHNSYEHMHNHLSQGLCR 102
OY 63 TCAYINRYQV--NCTATSNVAVCGCLPRFYRKTRIGLQ-----DQECTIPC----- 107
DB 103 PCDIVLFEFEVAPCTSDRKAC--RCQP-----GMSCVYLDNECVHCEERLYLQCP 152
OY 108 -TKQPTSEV-----OCAPOLSLVEADP-----T 131
DB 153 GTEAEVDELMDVDVNCVPCKPGHFQNTSPRARCPQHTACEIO-GIVEA-AGTSTSDT 210
OY 132 V---PQEGATLVALVSSLVVFTLALGLFLYCKQFNNH---CORGLDQPEADKTAK 185
DB 211 ICKNPPPGAMLLALITLISLVFLFTTV--LACA--WMHNPISCRKRLGTL-LKRHPEGE 265
OY 186 EESLFFPYP---PSKESAE-----SOVSWAPGSLAQLFSLDSVPIPOOQGP 229
DB 266 ESPPCAPRADPHFPDLAEPLLPMSGDLSPSPAGPPTAPSLAEVYL--QOQSP 316

```

RESULT 3
 TRIA_HUMAN STANDARD; PRT; 455 AA.
 ID TRIA_HUMAN
 AC P19438
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor 1 precursor (Tumor necrosis factor binding protein 1) (TNFR1) (p60) (TNF-R1) (p55) (CD120a).
 GN TNFRSF1A OR TNFR1 OR TNFRAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90235285; PubMed=2158863;
 RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Gatanaga T., Granger G.A., Lantz R., Raab H., Kohr W.J., Goeddel D.V.;
 RT "Molecular cloning and expression of a receptor for human tumor necrosis factor.";
 RT Cell 61:361-370(1990).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90235284; PubMed=2158862;
 RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M., Tschuch H., Lesslauer W.;
 RT "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.";
 RT Cell 61:351-359(1990).
 RL [3]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.
 RX MEDLINE=91006021; PubMed=1698610;
 RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R., Adlerka D., Holtmann H., Wallach D.;
 RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.";
 RT EMBO J. 9:3269-3278(1990).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91090841; PubMed=1702293;
 RA Hummler A., Maurer-Foy I., Kroenke M., Scheurich P., Pfizenmaier K., Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
 RT "Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";
 RT DNA Cell Biol. 9:705-715(1990).
 RL [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=91017509; PubMed=2170974;
 RA Gray P.W., Barrett K., Chantray D., Turner M., Feldman M.;
 RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
 RL [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92250049; PubMed=1315717;
 RA Fuchs P., Strehl S., Dworzak M., Hummler A., Ambros P.F.;
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to chromosome 12p13.";
 RT Genomics 13:219-224(1992).
 RL [7]
 RP SEQUENCE OF 41-45.
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";

RL J. Biol. Chem. 265:1531-1536(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
 RX MEDLINE=93258609; PubMed=8387891;
 RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J., Broger C., Loetscher H., Lesslauer W.;
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF beta complex: implications for TNF receptor activation.";
 RL Cell 73:431-445(1993).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX MEDLINE=97094982; PubMed=8939750;
 RA Natsumi J.H., Devine T.O., Rhoads H., Sprang S.R.;
 RT "Structures of the extracellular domain of the type I tumor necrosis factor receptor.";
 RL Structure 4:1251-1262(1996).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYTOTOXIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACID SPHINGOMYELINASE.
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SHASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SHASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SHASE.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- DATABASE: NAME=PROIM; NOTE=CD guide CD120a entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X55313; CAA39021.1; -
 DR EMBL: M33294; AAA03210.1; -
 DR EMBL: M58286; AAA36753.1; -
 DR EMBL: M63121; AAA36754.1; -
 DR EMBL: M75866; AAA61201.1; -
 DR EMBL: M75864; AAA61201.1; JOINED.
 DR EMBL: M75865; AAA61201.1; JOINED.
 DR EMBL: M60275; AAA36756.1; -
 DR EMBL: A21522; CAA01558.1; -
 DR PIR: A34899; GQHUT1.
 DR PIR: A35010; A35010.
 DR PIR: S12057; S12057.
 DR PIR: A38208; A38208.
 DR PDB: 1TNF; 3I-JUL-94.
 DR PDB: 1NCF; 07-DEC-95.
 DR PDB: 1EXT; 11-JAN-97.
 DR MIM: 191190; -
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 4.

```

DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR PROSITE: PS50017; DEATH_DOMAIN_1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
KW 3D-structure; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 455
FT CHAIN 41 291
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 455
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 338 348
FT DOMAIN 356 441
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHYD 54 54
FT CARBOHYD 145 145
FT CARBOHYD 151 151
FT VARIANT 305 305
FT CONFLICT 412 412
FT CONFLICT 443 446
FT SEQUENCE 455 AA; 50494 MW; 4CEFBFA96D03B8225 CRC64;

Query Match 11.4%; Score 145.5; DB 1; Length 455;
Best Local Similarity 21.3%; Pred. No. 1.7e-05;
Matches 66; Conservative 36; Mismatches 109; Indels 99; Gaps 14;

OY 3 COENEYWDGRCVTCQRCGPQDELSCDCGYEGGDVCTACPRRYKSMGH-HKQSC 61
DB 44 CPOGKIHPQNNISCTCKHKGTYIYNDGP-GPGQPTDCRECSGFTASENHLRHLCSC 102
OY 62 IRC-AVINRVQKVCATNSNAVCGDLPFRYRK----- 93
DB 103 SKCREMGVEISCTVDNDIVCG-CRKNQYRHVSENLFCPCNCSLCINGTVHLSCQEK 161
OY 94 ----TRIGG--LQDEICIPCTKQPTSEVQCAFQLSLEADAPVPOEAT-----L 139
DB 162 QNTVCTCHAGFLRENEVSCS-----NCKKSLECKKLPLQENVKGTEDSGTYVL 213
OY 140 VALVSSL-LVVTTLAFLGLFLYCK---QFNRHC-----QNGGLQEPADTKAESLE 190
DB 214 LPLVLVFFGLCLSLFLIGIMRYQRKSKLYIVCGKSTPEKEGELGTTPLAPNSF 273
OY 191 -----PYPSKETSAESQVSWAPGS-----LAQLFS 216
DB 274 SPTPGFTPLIGSPVPSSTFTSSS---TTPGDCPNFAAPRREVAAPYQADPILATIA 330
OY 217 LDSVPPIPOQ 226
DB 331 SDPIPNLPQK 340

```

```

DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-R1)
DE (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A.V., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific."
RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor."
RT Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91285014; PubMed=1647956;
RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,
RA Gray P.W., Feldmann M., Foxwell B.M.J.;
RT "Cloning, expression and cross-linking analysis of the murine p55
RT tumor necrosis factor receptor."
RT Eur. J. Immunol. 21:1649-1656(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE-Spleen.
RC MEDLINE=92039815; PubMed=1657766;
RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT "Molecular cloning and expression of the mouse tnfr receptor type b."
RT Immunogenetics 34:338-340(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245292; PubMed=8188324;
RA Bebo B.F., Lanthicum D.S.;
RT "Nucleotide sequence of the TNF type I receptor from a mouse
RT endothelioma cell line."
RT Immunogenetics 39:450-451(1994).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93156721; PubMed=8381516;
RA Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT "Genomic organization and promoter function of the murine tumor
RT necrosis factor receptor beta gene."
RT Mol. Immunol. 30:165-175(1993).
RN [7]
RP FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
RP RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
RP AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
RP PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
RP SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE
RP PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
RN [8]
RP SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
RP HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
RP PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
RP WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
RP PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
RP TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
RP ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
RP NF-KAPPA B SIGNALING (BY SIMILARITY).
RN [9]
RP SUBCELLULAR LOCATION: Type I membrane protein.
RN [10]
RP SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
RN [11]
RP SIMILARITY: CONTAINS 1 DEATH DOMAIN.
RN [12]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M60468; AAA39751.1; -
 DR EMBL: M59377; AAA40464.1; -
 DR EMBL: X59238; CAA41922.1; -
 DR EMBL: X5796; CAA40936.1; -
 DR EMBL: L26349; AAA59361.1; -
 DR EMBL: M76656; AAA40465.1; -
 DR EMBL: M80667; AAA40465.1; JOINED.
 DR EMBL: M76655; AAA40465.1; JOINED.
 DR PIR: A38634; GOMST1.
 DR PIR: S16677; S16677.
 DR PIR: S19021; S19021.
 DR HSP: P19438; 1EXT.
 DR MGD: MGI:1314884; Tnfstfla.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Receptor: Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 454
 FT DOMAIN 22 212
 FT TRANSMEM 213 235
 FT DOMAIN 236 454
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT REPEAT 197 349
 FT DOMAIN 350 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 151 151
 FT CARBOHYD 202 202
 FT CONFLICT 394 394
 FT SEQUENCE 454 AA; 50129 MW; 0710C2B8C3C2B6D9 CRC64;

Query Match 11.4%; Score 145; DB 1; Length 454;
 Best Local Similarity 21.9%; Pred. No. 1.9e-05;
 Matches 67; Conservative 37; Mismatches 112; Indels 90; Gaps 14;

QY 3 CQENYWDGRCVTCQRCGPQGLSKDYGSGDGYCTACPPRRYKSSWGH-HKQSC 61
 Db 44 CPGKTVHSSKNSICCTCKHKGTYLVSDP-SFGSDYVCRECKGFTASQNLRLQCLSC 102
 QY 62 ITC-AVINRQKVNCTATSAVCG-----DCLRFYKKTIT----- 96
 Db 103 KTRKREMSQVEISPCQADKDTVCCKENQFORYLSETHFQCVDCSPFCNGVTIIPCKETO 162
 QY 97 -----GG--LQDQECIPCTKQTPSEVQCAFQLSLVLEADAPLVPPQEAFLVALVSSL 147

Db 163 NTVCNCHAGFFLRSECVPSHCKNKE-----CKMLCPPLPLANTNPQDSG-TRVLLPLV 218
 QY 148 VETFLAFLGLFF-LYCK-----QFPNRHCQRCGLLQFEADKTAKEESLEFPVPSKETS 199
 Db 219 ILGLCLISLFTFISLMCRPRMRPEVYSIICR--DPVVKEEKKGRKLTTPAPSAFSPS 276
 QY 200 A-----ESQVSNAPGSLAOLF-----SLDSVP 221
 Db 277 GFNFTLGFSTPGFSSPVSSP--ISPIFGPSNMHMPVSEVPTGADPLLYESLCSVP 334
 QY 222 IPQ000 227
 Db 335 APTSVO 340

RESULT 5
 TNFR_MOUSE
 ID TNFR_MOUSE STANDARD; PRT; 250 AA.
 AC P41272;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 7 precursor (CD27L
 DE receptor) (T-cell activation antigen CD27).
 GN TNFRSF7 OR CD27.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=Thymus;
 RX MEDLINE=93209296; PubMed=8384562;
 RA Gravestein L.A., Blom B., Nolten L.A., de Vries E., van der Horst G.,
 RA Ossendorp F., Borst J., Loenen W.A.;
 RT Cloning and expression of murine CD27: comparison with 4-1BB,
 RT another lymphocyte-specific member of the nerve growth factor
 RT receptor family.";
 RL Eur. J. Immunol. 23:943-950(1993).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY
 CC -1- A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: IN THYMUS AND SPLEEN, BUT NOT IN NON-LYMPHOID
 CC TISSUES.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: L24495; -; NOT_ANNOTATED_CDS.
 DR PIR: A49053; A49053.
 DR HSP: P19438; INCF.
 DR MGD: MGI:88326; Tnfrsf7.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 KW T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat.
 FT SIGNAL 1 20
 FT CHAIN 21 250
 FT DOMAIN 21 182
 FT TRANSMEM 183 203
 FT DOMAIN 204 250
 CYTOPLASMIC (POTENTIAL).

```

FT REPEAT 26 63 TNFR-CYS 1.
FT REPEAT 64 104 TNFR-CYS 2.
FT REPEAT 105 141 TNFR-CYS 3.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 250 AA; 28164 MR; 48477C2E0C244697 CRC64;

Query Match 11.3%; Score 143.5; DB 1; Length 250;
Best Local Similarity 25.7%; Pred. No. 1.4e-05;
Matches 67; Conservative 22; Mismatches 97; Indels 75; Gaps 14;

QY 3 COENEMWDQRCVTCQRCGPGGELSDCGYGGGATCTACPRRYKSSWGHHK--COS 60
DB 27 CPBKHWGSGGGLC--CRMCEPGFEVFKDCEDORTA--AQCDPCIPGTSFSPDYTRPHCES 83
QY 61 CITCAVINRQKNCATATSNVAGDCLPRPYRRTIRIGLQDQDCTCTQTPSEVQCAF 120
DB 84 CHRNGSGFLIR--NCTVTANAE--SCSKMWQ-----CRDQCTEC---DPLPALTR 130
QY 121 QLSVEADAPTVPP-----QEAFLVALVSS---LILVPT 151
DB 131 OPS--ETPSPPPPHTLPHGTEKPSWPLHRQLPNSTVYSQBSHRPLGSSDCIRIFVTES 188
QY 152 LAFGLFLFYCKOFENRHCQRGGLQFEADKTAKESELP--VPSEKTSASQSVWAFG 209
DB 189 SMFL-LEVLGALIFHQRRNHGP---NEDROAVPEEPCPYSCPREESGA----- 234
QY 210 SLAQLFLSDVPPIQQOQGP 230
DB 235 -----IPQEDYRKPE 245

RESULT 6
TNFR6_PIG
ID TNFR6_PIG STANDARD: PRT: 332 AA.
AC 07736:
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
DE TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.; "Expression of apoptosis-associated genes in hibernating and stunned myocardium of pig.";
RT Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
RL -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

```

```

CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AJ001202; CA04596.1; -.
DR HSSP: P25445; 1DDF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00208; TNFR; 3.
DR SMART: SM00208; DEATH; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00650; TNFR_NGFR_2; 2.
DR PROSITE: PS0017; DEATH_DOMAIN; 1.
KM Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 332
FT DOMAIN 17 175
FT TRANSMEM 176 192
FT DOMAIN 193 332
FT REPEAT 45 81
FT REPEAT 82 125
FT REPEAT 126 164
FT DOMAIN 227 311
FT CARBOHYD 38 38
FT CARBOHYD 116 116
SO SEQUENCE 332 AA; 37592 MR; 588B03682756BFB1B CRC64;

Query Match 11.2%; Score 143; DB 1; Length 332;
Best Local Similarity 31.2%; Pred. No. 2e-05;
Matches 40; Conservative 15; Mismatches 53; Indels 20; Gaps 8;

QY 2 DQENEMWDQRCVTCQRCGPGGELSDCGYGGGADATCTACPRRYKSSWGHH--KCQ 59
DB 45 ECPESQNHRE--GQ--FCCPCPPGKRRHADG--TSPGAPQCVCSGEDYTKNHHSSKCR 100
QY 60 SCITCAVINRQV--KVCATATSNVAGDCLPRPYRRTIRIGLQDQDCTCT-----KQ 110
DB 101 RCRVDDSGHGLEVENKNCRTQNTK--RCKPNEFCHTS---QCEHCNCPCTTCEHGVLENC 155
QY 111 TPTSEVQC 118
DB 156 TPTSNKTC 163

RESULT 7
TNFR1_MOUSE
ID TNFR1_MOUSE STANDARD: PRT: 625 AA.
AC 035305;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-kB) (osteoclast differentiation factor receptor) (ODFR).
DE TNFRSF11A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Fetal liver;
RA MEDLINE=98032977; PubMed=93671155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Gallibert L.;
RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
RT Nature 390:175-179(1997).
RL [2]
RP FUNCTION.

```

```

RX MEDLINE-9909247; PubMed-9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RL differentiation factor in osteoclastogenesis."
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
CC -1- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL). ALSO KNOWN AS
CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF). ESSENTIAL FOR RANKL-
CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -1- TISSUE SPECIFICITY: UBICUITOUS EXPRESSION WITH HIGH LEVELS IN
CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF019046; AAB86810.1; -.
DR HSSP: P25942; 1CDF.
DR MGD: MGI:1314891; Tnfrrsf11a.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 625
FT -----
FT DOMAIN 31 214
FT TRANSMEM 215 234
FT REPEAT 235 625
FT REPEAT 35 69
FT REPEAT 72 113
FT REPEAT 115 152
FT REPEAT 155 195
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 128
FT DISULFID 134 152
FT CARBOHYD 106 106
FT CARBOHYD 175 175
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;

```

```

Db 205 PKRQAVLPISLIVLLFTISVVVAAIL-----FGYYRRKG 240
RESULT 8
ID TR14_HUMAN STANDARD; PRT; 283 AA.
AC 092956; Q9UM65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor
DE (Herpesvirus entry mediator) (Tumor necrosis factor receptor-like 2)
DE (TR2).
GN TNFRSF14 OR HVEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Cervical adenocarcinoma;
RA Montgomey R.L., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family."
RL Cell 87:427-436(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97306336; PubMed-9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA Porter T.G., Truneh A., Young P.R.;
RT "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation."
J. Biol. Chem. 272:14272-14276(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Gao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNFRSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.
CC PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED
CC THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO
CC CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (probable).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN LUNG, SPLEEN, AND THYMUS.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U70321; AAB58354.1; -.
DR EMBL: U81232; AAD00505.1; -.
DR EMBL: AF153978; AAF75588.1; -.
DR HSSP: P25942; 1CDF.
DR MIM: 602746; -.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_3.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 38
FT CHAIN 39 283
FT DOMAIN 39 202
EXTRACELLULAR (POTENTIAL).

```

FT TRANSMEM 203 223 POTENTIAL.
 FT DOMAIN 224 283 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 75 TNFR-CYS 1.
 FT REPEAT 78 119 TNFR-CYS 2.
 FT REPEAT 121 162 TNFR-CYS 3.
 FT DISULFID 42 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 111 BY SIMILARITY.
 FT DISULFID 99 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 138 162 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 17 K -> R (IN REF. 1).
 SQ SEQUENCE 283 AA: 30392 MW: 46CE13C2C70242C1 CRC64;

Query Match 11.1%; Score 141.5; DB 1; Length 283;
 Best Local Similarity 26.4%; Pred. No. 2.3e-05;
 Matches 63; Conservative 25; Mismatches 98; Indels 53; Gaps 14;

OY 3 COENETWDQMGKVCYQRCGPEQELSKDCGYEGGDAYCTACPPRRYKSSW-GHKQSC 61
 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11
 DB 42 CREDEY-PVGSBC--CPKSCPGYRKACGELTG--TVCEPCPGTYIAHLNGLSKLQC 96
 OY 62 ITC--AVIRVQKVNCTATSNVAGDCLP-----RFTY-----RKTIRIG 98
 DB 97 QMCDPAMGIRASR-NCSRTENAVCG-CPGHGCIYODGDHCAACRAVATSSPGQRYKGG 154
 OY 99 LQDQF-----CIPCTKQPTSEVQCAFOL--LVEADAPTVPEQATLVALVSLVVF 150
 DB 155 TESQPLCQNCPPGFSPGTFLECOHCKCSMLVTKAGAGTSSSHMWVWFLSGSLVIYI 214
 OY 151 TIAFLGLFYLKQKQFNRRCQRGGLQF-----EADTKAKEESLPFVPPSKETS 200
 DB 215 VCSYGL--TTC--VKRRKPRGDVYKVIIVSVQRKQAEAGATYIEALQAPPDYTV 268

RESULT 9

TNR6_BOVIN
 ID TNR6_BOVIN STANDARD: PRT: 323 AA.
 AC P51867.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
 DE (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96226401; PubMed=8634151;
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine Fas.;"
 RL DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: U34794; AAC48546.1; -.
 DR HSSP: P25445; 1DDF.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death_1.
 DR SMART: PF00020; TNFR_c6; 3.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR KMW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 FT CHAIN 1 16
 FT SIGNAL 1 16
 FT CHAIN 17 323
 FT SIGNAL 16
 FT POTENTIAL.
 FT TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 45 80 TNFR-CYS 1.
 FT REPEAT 81 124 TNFR-CYS 2.
 FT REPEAT 125 163 TNFR-CYS 3.
 FT DOMAIN 238 306 DEATH.
 SQ SEQUENCE 323 AA: 36445 MW: 4D8BA90E9E1F4892 CRC64;

Query Match 10.6%; Score 134.5; DB 1; Length 323;
 Best Local Similarity 26.2%; Pred. No. 0.00011;
 Matches 42; Conservative 19; Mismatches 70; Indels 29; Gaps 8;

OY 3 COENETWDQMGKVCYQRCGPEQELSKDCGYEGGDAYCTACPPRRYKSSWGHKQSC 62
 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11 1-1-11
 DB 45 COEGLYREHQ---FCCQCPPEKRRKNGDC-KRDGTPCVCVLSQENETDCKSHS-DKCI 99
 OY 63 TCAVINRVQ---KVNCTATSNVAGDCLPFRYKTRIRIGLQDQICPT-----KQ 110
 DB 100 RCSIQDEHGLEVEQNCITRTNTRKC-RKSNFF-----CNSPCEHCNPTCTGCHGIIK 154
 OY 111 TPTSEVQCAFOLSLVEADAPTVPEQATLVALVSLVVF 150
 DB 155 TPTSNTRKCKGRSHANS-----LMALLILLIPVILLITY 187

RESULT 10

TRIA_PIG
 ID TRIA_PIG STANDARD: PRT: 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor 1 precursor (p50) (TNF-R1) (TNF-R1) (p55).
 DE (p55).
 GN TNFRSF1A OR TNFR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96011645; PubMed=7590278;
 RA Suter B., Pauli U.H.;
 RT "Cloning of the cdna encoding the porcine p55 tumor necrosis factor receptor.;"

Query Match	10.6%	Score 134.5	DB 1	Length 461
Best Local Similarity	22.9%	Pred. No. 0.00015		
Matches 65; Conservative	40;	Mismatches 120;	Indels 59;	Gaps 14

CC COENZYME Q₁₀: A ubiquinol derivative involved in mitochondrial electron transport chain.
Dd CPGGKSHIPQANISICTCTCKHKSTYLIANDC-LDPGLDTRCEDNNGFTTASNNHLIQCLSC
102
Oy ITC-AVINRVOKNCVNTATSNMAGCDLPREFYRK-----TRIGILODEP-----IPCFO 110
Dd SKCRSEMSOVELSPCTVRDRPVCG-CRKNQKKRYNSEFLFQLNLCSLGNVTOLPCLEK 161
Oy ITPT-----SEVOCAFQSLSDVEADAPVPPO-----EATVALVSLLLVFTUL 152
Dd QDTIONCHSGGFELRDKECVSVCNCAKDCKNPATSETRNDFODTGTVLLPLIVIFGL 221
Oy AS-FLGLEFYLC---QEFNRRHQHG-GILQFEADAKTAEEES-----LFPPPSPE 197
Dd CLAFLEFGILLACRIQRMKPKLTITICGSTVKPEEPLEPAIAPSFGPIPTTFSSPIPSPSP 281
Oy TSASEOV-SMAPGSIAOLFSLD-----SVPIPDQQOGP 229
Dd TTTTSPPVPSFSPISSPTFTPCDMWSMIKYTSPEKETAPPQGAGP 325

RESULT 11

Trial Bovine STANDARD; PRt: 471 AA.

ID ID TRIA_BOVIN STANDARD; PRt: 471 AA.

AC 019131:

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-R1)
(p55).

GN TNFRSF1A OR TNFR1.

OS Bos taurus (Bovine).
Enxayrjola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
[1]

RN SEQUENCE FROM N.A.
RP TISSUE=Aorta;
RA Lee E.-K., Talvor M.J., Kehrl M.E.;
RT Cloning of cDNA encoding bovine tumor necrosis factor-receptor I
RT (TNF-R1). "

RL Submitted (Feb-1997) to the EMBL/Genbank/DDBJ databases.

CC -FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
PROTESSES) MEDIATING APOPTOSIS (BY SIMILARITY).

CC -SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NF-KAPPA B SIGNALING (BY SIMILARITY).

CC -SUBCELLULAR LOCATION: Type I membrane protein.

CC -SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC This SWISS-Prot entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb.ch/announce/
or send an email to license@isb.slb.ch).

EMBL: U90937 : AAB65143.1. -.
HSSP: P19438 ; 1TNR.
InterPro: IPRO00488 ; Death.
Interpro: IPRO01368 ; TNFR_C6.

```
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR Prodom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; signal; Apoptosis.
FT SIGNAL 1 21
FT CHAIN 22 471
FT DOMAIN 22 210
FT TRANSMEM 211 233
FT DOMAIN 234 471
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 195
FT DOMAIN 340 360
FT DOMAIN 372 457
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 190
FT DISULFID 185 194
FT CARBOHYD 54 54
FT CARBOHYD 145 145
FT CARBOHYD 151 151
FT SEQUENCE 471 AA; 51367 MW; 5243EF514DFE81C4 CRC64;
SO
Query Match 10.6%; Score 134.5; DB 1; Length 471;
Best Local Similarity 24.4%; Pred. No. 0.00016;
Matches 68; Conservative 26; Mismatches 120; Indels 65; Gaps 15;
QY 3 QGENEYWDGRCVYTCQRCGPGQELSKDCGYGEGDAYCTACPPRRYKSMGH-HKQSC 61
D 44 CPQKYNHPQNSTICCTCKHKGTYLYNDGP-GPRGDTDCRVCAFGTYALENHLRCLSC 102
QY 62 ITCA-VINRQKVCTATSNVACGDCLEPRYKRTIGLQDQECIPC-----TQOTPS 114
D 103 SRCRDEMFOVEISPCVVDRTVCG-CRKNQYRE-YWGETGFRCLNCISLCPNGTVNIPQ 159
QY 115 EVQ-----CAQQLSL-----VEADAPVP-----POEATLVALVSSL 146
D 160 ERDTICHCHGPFLLKAKKICSHDCKKKECEKICLPTPTSGKSQSDGTYLLPLV--- 216
QY 147 LVVF-TIAFLGLEFFLYCK-----QFPNRHCQGRGLLQFADKTAKESLFPVP---PS 195
D 217 -IVGICLICASVAVYLACRYQRMKPKLTSIIQGSTLV-----KKEBELLVPAQGFNP 270
QY 196 KETSAEQVSWAPGSLAQLESLD-----SVPLPQQQGP 229
D 271 TTICFSSPTSSSPVSIPIYICDSRNGFVAVASPSSETAP 309
RESULT 12
TNR3_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lymphotoxin-beta receptor precursor (Tumor necrosis factor receptor
  2 related protein) (Tumor necrosis factor C receptor).
GN LTRB OR TNFR OR TNFRF3.
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hccDNA library of human l2p
  transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=94252509; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
  IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L04270; AAA36757.1; -.
DR HSSP; P25942; ICDF.
DR MIM; 600979; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR Prodom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR Receptor; Transmembrane; Glycoprotein; Repeat; signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
FT SEQUENCE 435 AA; 46709 MW; 624526E6022F656F CRC64;
SO
Query Match 10.5%; Score 134; DB 1; Length 435;
Best Local Similarity 21.9%; Pred. No. 0.00016;
Matches 65; Conservative 29; Mismatches 109; Indels 94; Gaps 15;
QY 4 QGENEYWDGRCVYTCQRCGPGQELSKDCGYGEGDAYCTACPPRRYKSMGHK-COSCI 62
D 46 QEKYEYPOHR-ICCSRPFGTYVSAKC--SRIRDTVCATCAENSYNENHMTLITICQLCR 102
QY 63 TCAVINRQKV-NCVATSNVAC-----GDCLPRFYKRTIG-GL 99
```

Db 103 PCDPWGIEIAPCTSKRTQCRQPCAMALECTHCELLSDCPCTEALNKDEVK 162
QY 100 QDQCICP-----TKQPTSEVO-----CAFOLSTVEADAPT-----VPOE 136
Db 163 GNNHCVPCKAGHPONTSSSARCQPHRTCENO-GLVEAPAGRTAOSTTCKNPLEPPEK 221
QY 137 ATLVALVSSLVFTLAFGLFPLCKQKPFNNH---CQSGLLQFEADKTAKEESLPVP 193
Db 222 SSTMM---LAVLLPLAFPLLATVFSCKIMKSHPSLCRKLK-----SLKRR 265
QY 194 PSKETSASQSVSWAPGSLAQLF-----SLDSVP-----IPQOQ 226
Db 266 POGEGPNPVYAGSWEPKAPHPYDVLVQPLLPISGDVSPVSTGLPAPVLEAGVPOOQ 322

RESULT 13
TR1B_HUMAN STANDARD: PRT: 461 AA.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (TNFR1) (p80) (TNF-R2) (p75) (CD120b) (Etanercept).
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90260639; PubMed=2160731;
RX Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerry R., Dower S.K., Cosman D., Goodwin R.G.;
RA "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
RT Science 248:1019-1023(1990).
RL [2]
RN SEQUENCE FROM N.A.
RA MEDLINE=91045991; PubMed=2172983;
RX Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squitres C.H., Thompson R.C., Vannice J.L.;
RA "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RL [3]
RN SEQUENCE FROM N.A.
RA MEDLINE=96299745; PubMed=8661109;
RX Beltlinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepassier D., Stallard B.D., Goeddel D.V., Desauvage F.J.;
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RN SEQUENCE OF 116-461 FROM N.A. AND PARTIAL SEQUENCE.
RA MEDLINE=90349572; PubMed=2166946;
RX Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [5]
RN SEQUENCE OF 27-31.
RA MEDLINE=90110215; PubMed=2153136;
RX Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [6]
RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE=91056048; PubMed=2173696;

RA Loetscher H., Schlaeeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W., Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HU60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [7]
RN CHARACTERIZATION.
RA MEDLINE=93016040; PubMed=1328224;
RX Penica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH TNFR2.
RA MEDLINE=99221490; PubMed=10206649;
RX Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of human TNFR2.";
RL Nature 398:533-538(1999).
CC -I- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.
CC -I- PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to TNF-alpha and blocks its interactions with receptors.
CC -I- SIMILARITY: CONTRAINS 4 TNFR-CYS REPEATS.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC -I- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrelinfo.com/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sdb.ch/announce/> or send an email to license@sdb.ch).
CC -----
DR EMBL: M32315; AAA59929.1; -;
DR EMBL: M35857; AAA6362.1; -;
DR EMBL: U52165; AAC50622.1; -;
DR EMBL: U52156; AAC50622.1; JOINED.
DR EMBL: U52157; AAC50622.1; JOINED.
DR EMBL: U52158; AAC50622.1; JOINED.
DR EMBL: U52159; AAC50622.1; JOINED.
DR EMBL: U52160; AAC50622.1; JOINED.
DR EMBL: U52161; AAC50622.1; JOINED.
DR EMBL: U52162; AAC50622.1; JOINED.
DR EMBL: U52163; AAC50622.1; JOINED.
DR EMBL: U52164; AAC50622.1; JOINED.
DR EMBL: M55994; AAA36755.1; -;
DR PIR: A35356; A35356.
DR PIR: A36007; A36007.
DR PIR: A36475; A36475.
DR PIR: B35010; B35010.
DR PIR: A23666; A23666.
DR PDB: 1CA9; 12-APR-99.
DR MIM: 191191; -;
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF000020; TNFR_C6; 4.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;

Phosphorylation; Pharmaceutical; 3D-structure.

FT SIGNAL 1 22
FT CHAIN 23 461
FT DOMAIN 23 257
FT TRANSMEM 258 287
FT DOMAIN 288 461
FT REPEAT 39 76
FT REPEAT 77 118
FT REPEAT 119 162
FT REPEAT 163 201
FT DISULFD 40 53
FT DISULFD 54 67
FT DISULFD 57 75
FT DISULFD 78 93
FT DISULFD 96 110
FT DISULFD 100 118
FT DISULFD 120 126
FT DISULFD 134 143
FT DISULFD 137 161
FT DISULFD 164 179
FT CARBOHYD 171 171
FT CARBOHYD 193 193
FT CONFLICT 141 141
FT CONFLICT 196 196
FT CONFLICT 363 363
SO SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 10.4%; Score 132.5; DB 1; Length 461;
Best Local Similarity 21.2%; Pred. No. 0.00023;
Matches 71; Conservative 25; Mismatches 108; Indels 131; Gaps 15;

QY 3 COENFYMDQWGCVCPCGPGQELSKDCGVEGDAYCTACPPRRYKXSMGH-HKQSC 61
DB 40 CLRREYVQOTQO-MCSCSKCSRGQNAKVC--TKISDYCDSEDBSTYQJLNMWVECLSC 96
QY 62 ITCAVINRQVNCATATSNVAVCGDCLPRFY-----RKRTRIG-----G 98
DB 97 GSRCSDDVEQVQACTRQGNRIG-TCRPGWCALSKQEGCRICAPLRKCRPGVGVARPGE 155
QY 99 LQDECICTCTQCT-----YCKQFENRHQCRGLLQFEADKT-----AKESLFPVPPS 195
DB 156 TSDVVKCKCAGPTSNSTSSIDICRPHQICNVVAIPGNASRDVCTSTPSRMAPGAVH 215
QY 112 -----PTSEVOCAFQSLVEADAPTVPEOATL--VALVSLVVFPLAFGL 156
DB 216 LPQPVSTSQHTQPTPEPSTAPSTISFLPMGPS-PPABGSGTGFALPGLVGYTA--LG 272
QY 157 LFFL-----YCKQFENRHQCRGLLQFEADKT-----AKESLFPVPPS 195
DB 273 LLITGVNVCVIMTQVKKRPLCIQ-----REAKVPHLPADKARCTQGEQGHLLITAPSS 326
QY 196 KETSAESQVSNAPGSLADLFSLD-SVPIPQOQCP 229
DB 327 SSSSLSSAS-----ALDRRAPTRNOPAP 351

RESULT 14
ID TRIA_RAT STANDARD; PRT; 461 AA.
AC P22934;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-RI)
DE (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;

RA Himmler A., Maurer-Pogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantzi M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.:
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTOR DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (See <http://www.jsb-sib.ch/announce/>
CC or send an email to license@jsb-sib.ch).
CC -----
DR EMBL; M63122; AAA42256.1; -
DR PIR; B36555; B36555.
DR HSSP; P19438; INCF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR.1; 3.
DR PROSITE; PS00500; TNFR_NGFR.2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
KW SIGNAL 1 21
FT CHAIN 22 461
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 461
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 344 354
FT DOMAIN 363 448
FT DISULFD 44 58
FT DISULFD 59 72
FT DISULFD 62 81
FT DISULFD 84 99
FT DISULFD 102 117
FT DISULFD 105 125
FT DISULFD 127 143
FT DISULFD 146 158
FT DISULFD 149 166
FT DISULFD 168 179
FT DISULFD 182 191
FT DISULFD 185 195
FT CARBOHYD 34 34
FT CARBOHYD 151 151
FT CARBOHYD 201 201
SO SEQUENCE 461 AA; 50969 MW; BB23C05450FBD202 CRC64;

Query Match 10.2%; Score 130; DB 1; Length 461;
 Best Local Similarity 25.7%; Pred. No. 0.00038;
 Matches 53; Conservative 16; Mismatches 89; Indels 48; Gaps 10;

CC 3 COENEMYDQMGRCYTCORCPQELSKDCGYEGDAYCTACPPRRYKSSMGH-HKQSC 61
 DB 44 CPQGYAHKNNKSCCTCKHCKGYLVSDCP-SPQGETVCEVCDKGFYASQNHVRCQCSG 102
 QY 62 ITC-AVINRVOKVNCATATNAVCG-----DCLPFRYKTRT----- 96
 DB 103 KTCRREMFEVETSPCKADMDTVCGCKKNOFORLYLSETHRCVDCSPCFNGTVYIPCKERO 162
 QY 97 -----GG--LQDQECIPCTKOTPTSEVQCAFQSLVEADAPTVPQETVALYVSSLL 147
 DB 163 NTVCNCHAEFFLISGNCCTCTSCCKKNQF---CKKLCLPPVANYTNPQDSGTAVLLP---L 216
 QY 148 VVETLAFLG-LFPLYCKOFNHCQ 171
 DB 217 VI-----FLGLCLFFICISLRCRYPQ 238

RESULT 15
 ID TNF9_MOUSE STANDARD: PRT: 256 AA.
 AC P20334:
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
 GN TNFSF9 OR ILA OR LY63 OR CD137 OR CD157.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89184547; PubMed=2784565;
 RA Kwon B.S., Weissman S.M.;
 RT "CD4 sequences of two inducible T-cell genes."
 RT Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C.
 RX MEDLINE=94179805; PubMed=8133039;
 RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
 RT "Genomic organization and chromosomal localization of the T-cell antigen 4-1BB."
 RT J. Immunol. 152:2256-2262(1994).
 RN [3]
 RP CHARACTERIZATION, AND SEQUENCE OF 25-29.
 RX MEDLINE=93139510; PubMed=7678621;
 RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T., Kwon B.S.;
 RT "Inducible T cell antigen 4-1BB. Analysis of expression and function."
 RT J. Immunol. 150:771-781(1993).
 CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY ACTIVE DURING T CELL ACTIVATION.
 CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER. ASSOCIATES WITH p56-LCK.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
 CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch.

CC -----
 CC EMBL: J04492; AAA0167.1; -
 CC EMBL: U02567; AAA93113.1; -
 CC PIR: B32393; B32393.
 CC HSSP: P25942; 1CDF.
 CC MGI: M11059; Tnftrsf9.
 CC InterPro: IPR001368; TNFR_c6.
 CC Pfam: PF00020; TNFR_c6; 1.
 CC SMART: SM00208; TNFR_2.
 CC PROSITE: PS00652; TNFR_NGFR_1; 1.
 CC PROSITE: PS00500; TNFR_NGFR_2; FALSE NEG.
 CC Receptor: Glycoprotein; Repeat; Signal; Transmembrane.
 CC SIGNAL 1 24
 CC CHAIN 25 256
 CC FT 25 187
 CC FT 188 208
 CC FT 209 256
 CC FT 17 45
 CC FT 46 85
 CC FT 86 117
 CC FT 118 159
 CC FT 128 138
 CC FT CARBOHYD 138 138
 CC SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
 EXTRACELLULAR (POTENTIAL).
 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 9.
 POTENTIAL.

Query Match 10.2%; Score 129.5; DB 1; Length 256;
 Best Local Similarity 24.8%; Pred. No. 0.00023;
 Matches 66; Conservative 25; Mismatches 90; Indels 85; Gaps 13;

CC 16 VTCORCGPQELSKDCGYEGGDAY---CTACPPRRYKSSMGHKKQSCITCAVINRVOK 72
 DB 16 VGCEKGAVQNSCDNCQPGTFCRRKYNPVCKSPSTFSSIGQPNCNICVCGAFREKK 75
 QY 73 VNCATSNVAVCGDCLPFRY-----RKPRIIGLQDQF---C 104
 DB 76 F-CSSSTHNAEC-RCISGFHGLGPGQCTRCCKDCRPGQELTFOGCKTSLGTFNONGVGC 133
 QY 105 IPCTK-----QPTSE--VQC-----AFQSLVEADAPTVPP---QETL-VAL 142
 DB 134 RPTWNCISLDGRSVLKTGTETKEDVYCGPPVFSFSPSTTISVTPRGGPGHSLQVLTFLAL 193
 QY 143 VSSLVVFVTLAFLGLFPLYCKOFFNHCQNGGLQFADKTAEBESLFPVPPKETSABES 202
 DB 194 TSALL--ALIFTLLESVLKIWI-----RKKPHLIFKQPFKRTGA-- 232
 QY 203 QVSMAPGSLAOLFSLDSVPPIPOOOG 228
 DB 233 -----AQEDACSCRCPODEEG 249

Search completed: October 26, 2002, 21:09:13
 Job time : 13 secs

THIS PAGE BLANK (USPTO)